

Expectations of MMD under a model of genetic drift. S.N. BYERS, Department of Anthropology, University of New Mexico, Albuquerque, NM, 87131.

A study was performed of the expectations of the Mean Measure of Divergence (MMD) under the assumptions of genetic drift. Non-metric traits of the human skeleton were assumed to be controlled by individual alleles therefore making them subject to sampling errors from one generation to the next. The frequencies of these traits for a given skeletal series were entered into a computer program that randomly drew from an infinite number of alleles in proportion to these starting frequencies. The resultant count of traits then were used as starting frequencies of the next generation and the cycle was repeated. After a number of generations, MMDs were calculated between the starting and ending frequencies; and this simulation was repeated 1,000 times. This process was performed for a number of generations, using different starting frequencies and sample sizes, and different numbers of reproducing adults to arrive at an expected frequency distribution for this statistic. These expectations are presented and several real world examples are used to illustrate the utility of these simulations.

Testing a Hypothesis of Prehistoric Migration in Southeastern South America using mtDNA Haplogroup and D-Loop Sequence Variation. G.S. CABANA, (University of Michigan) F. ROTHHAMMER (University of Chile, Santiago, Chile) and D.A. MERRIWETHER (University of Michigan, Ann Arbor, MI),

We address the debate regarding the early peopling of southwestern South America using mtDNA RFLP and D-loop sequence variation. In particular, we test the hypothesis that early South American migrants traveled via an inland route into southwestern South America. Rothhammer & Silva (1992) specifically posit these prehistoric migrants settled in the highlands before subsequently peopling southwestern South America. In this case, these ancient migrations should account for the present-day pattern of genetic variation in this area. Modern descendants

of these founding and southwestern ancestral populations, then, should share more unique genetic mutations with each other than with other South American populations.

We test this hypothesis by using parsimony on mtDNA sequence data from modern native South American populations. We analyze sequence data from the HVSI portion of the D-loop from approximately 130 highland Aymara individuals and 200 southeastern Chilean individuals from the Huilliche and Pehuenche populations. Previous work (Merriwether 1993) on HVSI sequences from these same populations shows shared unique sequence variation among these three populations. Here we add HVSI data from these same populations. In addition, these data are evaluated against a background of sequence variation from surrounding South American populations (e.g., Ginther et al. 1993; Horai et al. 1993) to test the actual pattern of shared sequence variation between highland and southwestern populations and with other South American populations.

Inferring hominid behavioral adaptations during Okote Member times in the Koobi Fora region. S. CACHEL, J.W.K. HARRIS, C.M. MONAHAN, and M.J. ROGERS Anthropology, Rutgers University, New Brunswick, NJ 08901-1414, Sociology/Anthropology, Loyola University, Chicago, IL 60626, University of Nairobi, Nairobi, Kenya

A collaborative effort from 1997-1999 between Rutgers University and the National Museums of Kenya has yielded discoveries at two new bone modification sites east of Lake Turkana, in the Koobi Fora region of northern Kenya. The sites are in Okote Member deposits (1.64-1.39 mya) in the Koobi Fora Formation. These sites are FwJj 14 in area 1A at Ileret and GaJi 14 in area 103 at the Koobi Fora Ridge. These sites are relatively dense accumulations of surface and in situ bones with surface modifications and breakage patterns diagnostic of stone-tool using hominids. These finds nearly triple the current sample of well-preserved stone-tool modified bones from the Koobi Fora Formation. These sites occur outside the original focus area of the western escarpment of the Koobi Fora Ridge, which yielded the so-called "artifact mines"; they occur in different palaeoenvironmental contexts, in habitats which were probably marginal. Hence these sites also provide evidence of early Pleistocene hominid foraging and ranging behavior.

The high prevalence of cut-marks at FwJj 14, the density of the marks on individual bones, and the careful motor control necessary to produce such dense, fine marks all indicate Potts (1988) and Bunn (1994) emphasize that hominids butchering a carcass would encounter harassment and danger from sympatric carnivores, but these sites indicate that predator avoidance was not a problem for the hominids producing the zooarchaeological remains.

Archaeological survey which demonstrates alternative foraging strategies and complex foraging for dispersed resources implies intimate knowledge of the regional environment, and the ability to locate and predict the abundance of resources which fluctuate widely in space and time. The zooarchaeological evidence was presumably created by *Homo erectus* individuals. There may be profound differences between earlier taxa and later *Homo erectus*, and between sympatric hominid taxa. Given this evidence, Binford's (1984) routed foraging model of hominid sociality becomes questionable.

Censusing a primate community in Brazil: a multimethod approach. A.M Calouro¹, P.A. Garber², A. Stone², and W. de Aquino Chaves¹. ¹Departamento de Ciencias da Natureza, Universidade Federal do Acre, Brazil and ² Department of Anthropology, University of Illinois, Urbana, Illinois 61801

Accurate censusing of the number and density of primate groups living in a forest community is essential for developing successful policies of management and conservation. Among neotropical primates, problems of species' detection associated with small body size, behavioral crypticity, and limited visibility in dense vegetation can result in extreme variance in estimates of group size and number. In this paper we present data collected between February 1998 and May 1999 on the population densities of 8 primate species (*Callicebus cupreus*, *Callimico goeldii*, *Cebus albifrons*, *Cebus apella*, *Pithecia irrorata*, *Saguinus fuscicollis*, *Saguinus labiatus*, and *Saimiri boliviensis*) inhabiting Fazenda Experimental Catuaba, a 820 ha forest reserve administered by the Universidade Federal do Acre in northwestern Brazil (10°4' S, 67°37' W). Three censusing methods; line transect sampling (LT), concentrated area sampling (CA), and trapping, marking, and radiotracking of target study groups (TSG) were used in this analysis. LT samples were collected by walking a 14 km transect on each of 44 days. CA samples were collected by walking 6 km across a series of intersecting trails on each of 44 days. TSG data were collected over the course of 53 days on *Saguinus* and *Callimico* study groups that inhabited an area of approximately 110 ha.

LT sampling indicate species densities of from 0.4 groups/km² in *Callimico* to 3.0 groups/km² in *Saguinus fuscicollis*. Except for *Saimiri*, group size and group spread did not appear to markedly effect the frequency of species' sightings. CA sampling adjusted for species differences in home and day range size, and degree of home range overlap resulted in higher population density estimates for all species except *Saimiri* and *Saguinus fuscicollis*. Based on trapping and radiotracking of marked callitrichine groups (TSG), the density of *S. fuscicollis* and *S. labiatus* was found to be 30-60% greater than estimated with either LT or CA sampling. The strengths and weaknesses of each of the three sampling methods are discussed. We argue that the use of a multi-method approach is most advantageous when censusing primate species that differ significantly in behavior, body size, group size, home range size, and group spread.

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Factors influencing weight and BMI variability between 20 and 55 years of age. NOEL CAMERON and CARL BEYNON, Department of Human Sciences, Loughborough University, Loughborough, UK

In view of the association between body weight, weight variability, BMI and increased risk factors for a variety of non-communicable diseases in middle age, it would be useful to be able to predict weight changes from known physical status in early adulthood. The Loughborough Alumni Health Study (LAHS) is a follow-up study of 1179 males who were morphologically assessed at entry to university between 1958 and 1967. One hundred and one of the respondents have subsequently been re-assessed in 1999 30 to 40 years after their initial examination. The current analysis investigates the morphological variables in early adulthood that predict subsequent weight and BMI changes. Mean weight gain was 12.00kg (SD = 8.18kg) and weight change per annum varied from -0.15 kg.yr⁻¹ to 1.08 kg.yr⁻¹ with a mean of 0.34 kg.yr⁻¹ (0.24 kg.yr⁻¹). 97% of participants gained weight with 43% becoming "overweight" (BMI>27) and about 15% becoming "obese" (BMI>30) at follow-up. Significant associations were exhibited between weight change (whether total or per annum) and initial weight, subscapular, suprailiac and abdominal skinfolds, bi-epicondylar femur, flexed arm girth and waist girth. Flexed arm girth combined with abdominal skinfold provided the best two-variable combination to predict weight change with a multiple R of 0.532 (p<0.001; R²=0.283) and arm girth was the *single* best predictor, R = -0.481 (p <0.001 R²=0.232). The initial combination of significant independent variables implies that fat patterning has an important role in weight gain from young adulthood to middle age. However, those who will eventually become overweight or obese cannot be easily identified from morphological variables in early adulthood. At follow-up significant differences existed between the three groups for all variables except height and bi-acromial diameter. In particular the obese group had gained an average of 21.9 kg in weight compared to 7.6 kg and 15.7 kg for the other groups. Of this weight gain in the obese group, approximately one third was composed of lean body mass and two-thirds of fat compared to a weight gain in the normal group composed almost entirely of increased fat mass.

Population Variation in Age-Related Decline of Salivary Testosterone and Its Relationship to Body Composition B. CAMPBELL, Boston U, Boston, MA 02215, P. ELLISON, S. LIPSON, M. O'ROURKE, Harvard U, Cambridge MA 02128, R. BRIBIESCAS, Yale U, New Haven CT 06520, A. UCHIDA Chiba U, Chiba, Japan, G. JASIENKJ, Jagiellonian U. Krakow, Poland

Testosterone (T) has been associated with both aging and body composition among males. It is unclear, however ; 1) the extent to which T decline represents an

inevitable aspect of senescence; 2) the relationship of T declines to age-related changes in body composition. To determine the degree to which declines in T and its association with body composition are population specific we sampled men from five populations.

Sites included urban areas in the U.S. Japan, Poland, Venezuela and Zimbabwe, with roughly 80 subjects ages, 30-80, at each site. Salivary samples, collected both morning and evening for two days, were assayed for T. Anthropometric measures including height, weight, waist circumference and skinfolds measures were obtained.

Average morning (am) T levels varied across the five populations, with Poland (213 ± 112 pmol/L), significantly higher than U.S (186 ± 77), Zimbabwe (172 ± 81), Japan (141 ± 77) and Venezuela (148 ± 83). Both am and pm T values varied by age. am T values showed a significant site by age interaction, indicating a different rate of decline across sites, with higher average values associated with a greater rate of decline.

Height, BMI, waist circumference, and FFM varied across populations. Both waist circumference and FFM were significant predictors of pm T levels, controlling for age and population.

These results 1) confirm the existence of significant population differences in salivary T using a single assay technique; 2) demonstrate populations differences in the rate of age-related decline in T; 3) are consistent with clinical work indicating that T is related to measures of abdominal fat; 4) provide evidence for the hypothesis that T is related to population differences in skeletal muscle mass.

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A behavioral and hormonal investigation of female directed male aggression in free-ranging black-handed spider monkeys (*Ateles geoffroyi*). C.J. CAMPBELL, Department of Anthropology, University of California, Berkeley, CA 94720.

Male spider monkeys (genus *Ateles*) have been observed to "attack" females, in what often seems to be a cooperative manner. Two main hypotheses have been proposed to explain this aggression. Male attacks may cause females such distress that they urinate or defecate, providing a means to determine female reproductive status through olfactory cues in the urine and/or feces. Alternatively, the behavior may function as a form of sexual coercion increasing a male's ability to gain reproductive access to cycling females.

During a 15 month study of the reproductive biology and behavior of black-handed spider monkeys (*Ateles geoffroyi*) on Barro Colorado Island, Panama, 100 such attacks were observed during more than 1,200 hours of observation. Only 4 attacks resulted in

observed defecation/urination, and in only 24 cases were males observed to place sniff areas where the females had been sitting, strongly refuting the first hypothesis. Cycling females, as determined by fecal steroids (E1C and PdG), received the majority but not all of the attacks. The timing of attacks in relation to the periovulatory periods of cycling females will also be discussed. The number of attacks performed by a male was not positively related to the number of copulations he was involved in, suggesting that sexual coercion may not fully explain this behavior. This research was supported by grants from the L.S.B. Leakey Foundation and the National Science Foundation (SBR-9711161).

Limb proportions in modern Portuguese known sex and age skeletal samples. H. CARDOSO, S.N.WASTERLAIN and E.CUNHA, Departamento de Antropologia, Faculdade de Ciências e Tecnologia, Universidade de Coimbra, 3000-056 Coimbra, Portugal.

To understand the significance of limb proportion indices of fossil populations, it is important be aware of patterns of variation in recent populations. Here we review evidence for the brachial, crural and intermembral indices in a large series of known age and sex individuals from late 19th and early 20th Portuguese cemeteries. Using 400 identified skeletons deriving from two different collections [Lisbon (N=200) and Coimbra (N=200)], we evaluated sex and sample variation in the brachial, crural, and intermembral indices by univariate and residual analysis. Within each series, the brachial and intermembral indices show statistically significant differences between sexes. On the other hand, when comparing the two samples, the female crural index is the only one showing statistically significant differences between the two samples. Overall, females tend to have shorter forearms than males, while their legs are longer in relation to the arms, compared to males.

These results are just preliminary since in a near future they will be applied to a Middle Pleistocene series.

Chronic Vitamin C Deficiency as an Important Factor of Morbidity and Mortality in Prehistoric Populations.

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The diagnosis of chronic scurvy in archaeological skeletal remains by macroscopic analysis only is not reliable. As subperiosteal bony structures are also caused by various other diseases such as inflammatory processes, microscopic investigations are necessary. In dry bones, the main features caused by chronic scurvy are subperiosteal new bone formations representing mineralized hemorrhagic processes. Such alterations are frequently found on the shaft of the long bones, on the skull vault, and in the jaw area. In subadults, these pathological changes are usually much better expressed because in this age group bone metabolism is more active. There is a close connection between scurvy and other diseases such as posthemorrhagic anemia. Additionally, scurvy is able to create an immunodeficiency. Thus, infectious diseases are consecutively seen.

With regard to nutrition, prehistoric populations were strongly dependent on their environment. In Neolithic times, subsistence was mainly based on agriculture. Cereals such as corn or wheat provide no vitamin C, and fruits and vegetables were available only at certain time of year. During wintertime, the adequate supply with fresh food was probably difficult. Thus, a seasonal deficiency of vitamin C should be considered. In Neolithic child populations from Central Europe scurvy was observed in different frequencies with a range of 6.7-35%. In the adults the frequency was apparently lower. In child populations of the Early Bronze Age from Central Europe and northern Anatolia, frequencies with a range of 0.0-21.4% were observed.

How modal are positional behaviors - application of a new methodology, Labanotation, in the study of primate behavior? K.J. CARLSON, Department of Anthropology, Indiana University, R. HARDIWAY, North Carolina State University, Raleigh, NC, 27695, C. HOLLADAY, F. KNAPCZYK, J. SATKOSKI, S. SCHUCK, and G. THOMAS, Indiana University, Bloomington, IN, 47405.

Over thirty years ago, Pross defined positional behavior as "the study of how and when an animal establishes particular spatial relations between his body mass and his physical environment". Recently, Hunt and colleagues presented a standardized scheme for categorizing positional behaviors into 32 modes with 126 sub-modes. We present Labanotation as a complimentary methodology, one which is not based upon assigning movements to categories, but rather, displays a language-like characteristic of openness in combining symbols to capture body poses.

In 1928, Rudolf Laban devised, as a system of movement

notation, Labanotation for recording dance movements. Symbols depict body segments and joints, including their degrees of rotation, flexion, and extension. The system also highlights segments supporting body mass. Such detail in data recording facilitates biomechanical investigations. Additionally, Labanotation has tremendous potential for improving our understanding of non-verbal communication between primates (e.g., display behaviors).

Between May and July 1999, using standard positional behavior methodology (i.e., that of Hunt and colleagues), we collected 2322 instantaneous focal observations of *G. g. gorilla* and *P. paniscus* positional behavior from apes at the Cincinnati Zoo. We simultaneously video recorded these individuals and gathered approximately 400 instantaneous focal observations using Labanotation methodology. We have an additional 100 instantaneous focal observations using Labanotation methodology without video recording.

Labanotation data indicates that some positional behaviors are truly modal, while others appear less so. Comparing a subject's location of body mass support during a positional behavior, locomotor behaviors demonstrate little variation in support configuration, while postural behaviors demonstrate significantly more variation in support configuration. We suggest that generally greater stresses generated during locomotor behaviors restrict freedom in positioning body supports more so than during many postural behaviors.

Human Longevity: Nature vs. Nurture ~ Fact or Fiction. B. A. CARNES, National Opinion Research Center, and Center on Aging, University of Chicago, Chicago, IL 60637

Methods of estimating heritability were developed by geneticists in order to monitor their progress in making improvements to attributes of plants and animals that were of potential economic importance to agriculture. The concept of heritability, if not always the mathematics, has also been applied to human longevity. Raymond Pearl wrote classic papers on this topic during the 1930s and Karl Pearson, the famous statistician, published a paper on human longevity in 1901. In the first half of the century, heredity was considered an important contributor to human longevity. As the 20th century comes to a close, life expectancy has reached unprecedented levels in developed nations. Huge investments have been put into the Human Genome Project and the biomedical sciences have made phenomenal progress in the treatment of human disease. Interestingly, as more genes that cause disease are identified, researchers from a variety of disciplines are coming down on the nurture side of the nature versus nurture debate on human longevity. Should the methods and assumptions used to calculate heritability even be applied to longevity? Does a low heritability mean that genes have very little influence on longevity? Diseases linked to free radicals generated by normal metabolic pathways makes it impossible to provide a definitive answer to these questions at this time.

The running-fighting dichotomy and hominid evolution. D. R. CARRIER, Department of Biology, University of Utah, Salt Lake City, Utah 84112.

Characters that facilitate fighting often conflict with those that enhance locomotor stamina. Some of the characters which distinguish *Australopithecus* and *Homo* (e.g., limb length, proportions, and robustness) may reflect a dichotomy between selection for fighting versus locomotor stamina.

We are studying functional tradeoffs between fighting and running by comparing two breeds of domestic dog that have experienced strong selection for fighting (Pit Bulls) and running (Greyhounds). These breeds exhibit significant differences in their i) metabolic cost of transport; ii) capacity to store and recover elastic strain energy when running; iii) relative size of heart, spleen, and testes; iv) thickness of skin; v) trunk length and shape; vi) robustness of head, neck, and thorax; vii) position of center of mass in trunk; viii) limb length; ix) relative fore and hindlimb distribution of muscle mass; x) proximal to distal distribution of muscle mass in the limbs; xi) relative bone strength in fore versus hindlimbs; xii) relative bone strength in proximal versus distal limb; xiii) stress and strain at which limb bones fail; and xiv) modulus of elasticity of bone tissue.

The level of sexual dimorphism in body size has been interpreted to reflect moderate to high intensity male competition in australopithecines and lower levels of male competition in early *Homo*. Our analysis of dogs leads us to suspect that the fossil record will hold additional clues to the relative intensity of male competition: i) muscle mechanical advantage; ii) size and robustness of fore versus hindlimbs (McHenry, 1996); iii) robustness of proximal versus distal limb bones; iv) robustness of ribs; v) robustness of vertebral articulations; and vi) modulus of elasticity of bone tissue.

Homo is characterized by features that are believed to increase locomotor stamina. Invention of improved weapon technology in the lineage that gave rise to *Homo* may have reduced the conflict between selection for locomotor stamina versus male competition, and allowed a greater independence in the evolution of characters associated with locomotor stamina. Weapon technology may have opened new avenues for cursorial specialization in *Homo*.

A preliminary analysis of the relationship between osteoarthritic lesions and cross-sectional geometry as a determination of activity patterns among the prehistoric agriculturalists of Arroyo Hondo Pueblo, New Mexico. E.A. CARSON, M.A. SCHILLACI, and M.L. RHOADS, Department of Anthropology, University of New Mexico, 87131.

Osteoarthritic lesions have been interpreted as representing degenerative change caused by increased

activity levels or unusual loading patterns (e.g. Knusel, 1993; Bridges, 1993). Few studies have actually examined the direct relationship between patterns of the development of osteoarthritis and mechanically relevant cross-sectional data. This study compares the cross-sectional geometry of the humerus, femur, and tibia with osteoarthritic lesions in the prehistoric agricultural Arroyo Hondo population to determine whether osteoarthritis is related to increases in axial loading, as indicated by cross-sectional cortical area (CA) or by bending stress indicated by second moments of area (I_{max} , I_{min}).

We examined the remains of 32 adults from Arroyo Hondo Pueblo in New Mexico (AD 1300-1425). Osteoarthritic lipping and eburnation were scored for each vertebral and long bone joint surface preserved. Complete long bones were preserved for 29 of these individuals, allowing us to obtain CT scans for measuring the mechanically relevant cross-sectional properties for individual elements. Assuming that osteoarthritis is a good indicator of increased activity levels, we expected higher frequencies of osteoarthritic lesions on those elements associated with the greatest mechanical loadings.

We also documented the occurrence of osteoarthritic lipping and eburnation on the zygapophyseal joints of each preserved vertebral element from the Arroyo Hondo population. These results were then compared with the biomechanical loadings and osteoarthritic lesions observed on long bones to determine whether increase activity levels in the lower or upper extremities would differentially affect various regions of the vertebral column.

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Symposium introduction. Charles Oxnard: an appreciation. M. CARTMILL, Biological Anthropology and Anatomy, Duke University, NC 27710.

In an extraordinary scientific career extending across the entire second half of the 20th century, Charles Oxnard has placed his unique stamp on virtually every aspect of our discipline and has influenced the growth and direction of biological anthropology on four continents. Although his meticulous early work in descriptive comparative anatomy stands as an exemplar of the classical tradition, Oxnard has been still more influential as a pioneer of novel metric and analytic methodologies. As a primatologist, he has used these techniques and technologies not only to illuminate the functional anatomy and biomechanics of the primate skeleton, but also to develop new approaches to phylogenetic reconstruction in which subjective verbal descriptions are supplanted by quantitative assessments of morphology. As a paleoanthropologist, Oxnard had the courage to uphold a minority

view of the australopithecines throughout his career, and has been rewarded in recent years by a gradual (if unacknowledged) acceptance of most of his key ideas into the current consensus. Oxnard's unexcelled inventiveness, scientific rigor, keen enthusiasm, and genial good humor have made a lasting impact on all of us who have had the pleasure and privilege of studying under him or working with him during the past half-century. The example he has set as a teacher, mentor, and colleague will be one of his most far-reaching legacies.

Vertebral Osteophytosis / Degenerative Disc Disease (VO/DDD) in the rhesus monkeys of Cayo Santiago.
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Degenerative changes of the spine have a high prevalence in human populations, and are almost ubiquitous among older individuals. Spontaneous VO/DDD was studied in a sample of complete, macerated spines from the CPRC Museum collection from Cayo Santiago, Puerto Rico. VO/DDD was scored macroscopically, using an ordinal scaling system. Patterns by age/sex, parity and by amphiarthrodial (AAR) joint across the spine were assessed. VO/DDD is present in relatively high frequencies in both sexes. Thirty-six percent of individuals (N = 204) exhibit some degree of VO/DDD, from a spinal average score of 1 (mild) to 4 (severe), and there is no significant difference in frequency between the sexes. VO/DDD increases in severity with age, and there is no effect on parity. Degenerative changes begin at ~ 8-10 years of age. All individuals older than 15 years exhibit some degree of VO/DDD. In rhesus monkeys, VO/DDD has a predilection for the thoracic spine, which accounts for a significant proportion of the variance (69.3%) in the total sample of 5,304 AAR joints. The disease is most prevalent in joints T5/T6 to T12/L1 inclusive. The distribution of VO/DDD appears to reflect the normal curvatures of the macaque spine. For example, the thoracolumbar junction is subjected to unique biomechanical stresses due to its position at the apex of curvature of the macaque spine. This site also exhibits some of the highest scores and frequencies of VO/DDD. The thoracic vertebrae, transitional thoraco-lumbar region and L7/S1 tend to exhibit the highest frequencies of all grades of VO/DDD. Female and male rhesus monkeys exhibit similar frequencies, and similar patterns by age/sex and joint distribution. In contrast, the lumbar region of the human spine is most susceptible to VO/DDD, and human males have a higher prevalence of disc degeneration than do human females.

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Ascertainment bias of control samples in studies of the genetics of aging. R. CHAKRABORTY, O. SCHWALB, P. OLOFSSON, and M. KIMMEL. Human Genetics Center, Univ. Texas School of Public Health, Houston, TX and Dept. Statistics, Rice University, Houston, TX.

Indicators of genetic influence on longevity include familial aggregation of aging and association of genetic polymorphism with inter-individual variation of life-span. Demonstration of familial aggregation requires comparison of life-spans of relatives of long-lived probands and individuals randomly chosen from the population. Likewise, genes associated with aging are identified by comparative analyses of candidate loci between gene pools of extremely elderly and younger persons from the same population. Genetic influences on aging are supported by both approaches, indicating moderate heritability (23% to 26%) of longevity and influences of genes such as apolipoprotein B (APOB) and tyrosine hydroxylase (THO). Since longevity is influenced by birth-cohort, questions arise with regard to the suitability of a control sample defined by the younger persons from the contemporary population. Historical prospective studies of life-span are of limited value, since such studies can only be conducted in a few populations. Further, detailed genetic analyses of deceased individuals of the same birth-cohort are almost impossible.

We develop a statistical methodology through which the contemporary population can be used as a source of the control sample, adjusting for the birth-cohort effect on longevity. This sampling problem is formulated in the framework of biased age distributions in a general branching process. Using the theory of random characteristics of age-dependent branching processes, the bias of the age distribution is evaluated when individuals are sampled from different birth-cohorts. The implications of this theory are discussed in relation to the reported prevalence of centenarian siblings of centenarian probands (approximately 2%) as opposed to the estimate (1 in 6,000-8,000) in the contemporary US White population. This theory is also relevant for interpreting data on associations of genetic polymorphism with aging. (Research supported by NIH grants GM 41399, GM 45861 and GM 58545).

An expanded linkage map of chromosome 20 (PHA20) in the baboon (*Papio hamadryas*). K.E. CHAMBERS, D.E. NEWMAN, M.C. MAHANEY, P.A. MORIN, J. ROGERS. Dept. Of Genetics, Southwest Foundation for Biomedical Research, San Antonio, Texas, 78245.

In collaboration with Axys Pharm. Inc. (La Jolla, CA), a linkage map consisting of 331 microsatellite markers has been constructed for all baboon autosomal chromosomes. This map

was developed using genotype data from 694 outbred, pedigreed baboons at the SW Fndtn for Biomed. Res. We report the addition of three markers to the linkage map of baboon chromosome 20 (PHA20), which is homologous to human chromosome 16 (HSA16). These markers will fill previously sparsely mapped regions of the chromosome.

A chromosomal linkage map represents the relative positions of genetic polymorphisms or "markers" along the length of a chromosome. Nine human microsatellite markers have been mapped to unique positions on PHA20 with statistical support of 100:1, indicating that this order of loci is 100 times more likely than any other order. Compared to the Marshfield, Genethon and CEPH/Genethon human linkage maps, marker order is mostly conserved between species except for the inversion of markers D16S401 and D16S403. A tenth marker was mapped to a region spanning two intervals in the ordered map, the position of which is consistent with the human marker order. These maps can be used to compare chromosome structure and content among species and to locate the positions of new genes in relation to the markers.

The effects of gene flow on phylogenetic analysis using cladistic methodology.

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Cladistic perspectives have enjoyed an ongoing popularity in paleoanthropological studies ranging from examinations of australopithecine phylogeny to the origin of modern humans (Lieberman, 1995). However, the application of cladistic methods has been criticized on a number of grounds. In particular, there are questions about the efficacy of cladistics below the species level because of the confounding effects of gene flow between terminal taxa predicted by certain models of human evolution.

A recent study explored the use of cladistics to analyze intraspecific variation among populations of *Cercopithecus aethiops*, a well-studied, wide-ranging species complex with a number of recognized species and subspecies (Chang 1999). A cladistic analysis of 90 skeletal specimens divided into 11 taxa using 30 craniodental characters (12 discrete, 18 continuous) resulted in poorly resolved phylogenies demonstrating high levels of homoplasy. Because cladistic methods are also sensitive to the treatment of data - selection and coding of characters, construction of taxa, and choice of outgroups - it is important to distinguish between the effects of gene flow and methodological factors. While the former indicate that the use of cladistics is inappropriate, the latter simply suggest that it is difficult to apply.

The present study examines the effects of gene flow on phylogenetic analysis, and compares these effects to those

related to the construction of the analysis. The original data set was revised and expanded, and phylogenies generated using PAUP 3.1.1 and MacClade 3.08. The effects of gene flow were controlled in two ways: first, geographically-intermediate samples were eliminated under the assumption that proximity is related to levels of gene flow; second, where possible, levels of gene flow were estimated using molecular data and the published methods of Slatkin and Maddison (1989) and Hudson et al. (1992).

The results of analyses for which gene flow was controlled were compared to separate analyses utilizing alternative methods of treating data. These comparisons indicate that while gene flow has a significant effect on the outcomes of phylogenetic analysis, methodological factors have an even greater effect. The implications of these results for the application of cladistic method to intraspecific phylogeny are discussed.

Historical biogeography of the gibbons. H. CHATTERJEE, M. COLLARD, L. C. AIELLO and M. THOMAS, University College London, WC1E 6BT, UK.

The gibbon genus *Hylobates* comprises eleven species that are widely distributed across mainland and archipelagic Southeast Asia. Some of the species are geographically isolated (e.g., *H. moloch*), others have distributions that come into contact (e.g., *H. lar* and *H. agilis*). Currently, little is known about the processes that have led to this pattern of distribution. To rectify this situation, we have carried out a dispersal-variance analysis (F. Ronquist, Syst. Biol. 46, 195-203 [1997]) of the gibbons.

In the first part of the study, morphological and molecular data were used to estimate gibbon phylogeny. The morphological data comprised measurements of the cranium, dentition and postcranium. One of the Mosimann family of shape ratios was used to adjust the morphological data for the confounding effects of body size. The size-adjusted morphological data were converted into discrete character states using segment coding (R. S. Thorpe, *Evolution* 38, 244-355 [1984]). The molecular data consisted of original sequences for the mitochondrial control region and published sequences for cytochrome b gene (M. Hall et al., *Mol. Phyl. Evol.* 10, 281-286 [1999]). The data sets were analysed using the phylogeny reconstruction program PAUP 3.0s (D. L. Swofford, Illinois Natural History Survey, Champaign [1991]).

In the second part of the study, the estimate of gibbon phylogeny was combined with distribution data, and analysed using DIVA 1.0 (F. Ronquist, http://www.systbot.uu.se/staff/f_ronquist/f_ronquist.html [1996]), which uses a parsimony algorithm to estimate the number of vicariance, dispersal and extinction events that are required to explain the distribution of a set of taxa. The resulting dispersal-variance hypothesis was then compared to published biogeographic hypotheses for the gibbons.

This study has provided a novel reconstruction of the historical biogeography of gibbons. In addition, the cladistic analysis of morphological and molecular data has shed light on the controversial topic of hylobatid phylogeny.

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Estimating genetic relationships within primate populations using molecular genetic data. J. M. CHEVERUD¹, J. ROGERS², and P. MORIN³. ¹Dept. of Anatomy & Neurobiology, Washington University, St. Louis, MO 63110. ²Dept. of Genetics, Southwest Foundation for Biomedical Research, San Antonio, TX 78284. ³Axys Pharmaceuticals, South San Francisco, CA, 94080.

The recent upwelling of highly polymorphic molecular markers has raised the possibility that such markers can be used to reconstruct genealogical relationships among members of feral primate populations. Recent theoretical advances have also improved the efficiency of relatedness estimates based on molecular markers.

Over 300 polymorphic microsatellite markers have been identified in baboons at the Southwest Foundation for Biomedical Research by testing markers known to be polymorphic in humans. We used two sets of markers, a highly polymorphic set and a set with low polymorphism to reconstruct genealogical relationships among pedigreed animals from the Southwest Foundation for Biomedical Research. We have estimated the genetic correlation between individuals using the molecular markers and regression methods and then compared these estimates to expected genetic correlations obtained from the genealogies.

Overall, we found a fairly strong relationship between relatedness as measured with molecular markers and genealogies. However, the sampling error of the interindividual genetic correlation estimates was fairly high. While the average relatedness of a class of relatives is near the expected value, individual estimates cover a wide range. Various alternative algorithms are suggested to reduce estimation errors.

Measures of genetic relatedness are potentially of great use in behavioral ecology and quantitative genetic research. The relatively large amount of sampling variance for molecular-based estimates of genetic relatedness has different consequences in these two fields and is likely to be more of a problem in behavioral ecology research.

Forensic and Anthropological Aspects of Variation in Dental Metrics in Two Contemporary Australian Populations. ALISON L.S. CHIU, Department of Anatomy & Histology, The University of Sydney, Australia 2006.

The ability to discriminate between the major ethnic groups (Caucasoid and Mongoloid) in the Sydney region of Australia based on dental dimensions is extremely valuable in the forensic identification of individuals. Furthermore, metric variation in the dentition of these contemporary populations is poorly understood in this region of the world. As both the forensic and anthropological utility of this feature is presently unknown, this study examines the value of variation in tooth dimensions in discriminating between these two groups.

Dental stone casts of the permanent maxillary and mandibular dentition of 200 individuals were made and mesiodistal and buccolingual crown dimensions were

recorded for each tooth. Both univariate and multivariate analyses were used to investigate differences in linear and areal dimensions as well as the predictive value of these measures in a forensic context, using discriminant function analysis (DFA). DFA produced separation of Caucasoids and Mongoloids with a success rate of 93.9% on the basis of these measurements. Separation of the groups was most apparent in the mesiodistal and buccolingual dimensions of the P³, the mesiodistal diameter of the P⁴ and the mesiodistal dimension of the P₃. Interestingly, it was also possible to separate males from females within each ethnic group, with a success rate of 77.3%. The variables contributing to the discrimination of males and females include the mesiodistal and buccolingual dimensions of the M¹ and mandibular canine, and the mesiodistal dimensions of the M₁ and M₂.

This research presents, for the first time, metric data recorded from the dentitions of the major ethnic groups living in the Sydney region. The results from this study further highlight the usefulness of dental metrics in forensic applications and contribute to our knowledge of the variation of these features in contemporary human populations.

Evolutionary patterns and processes in New World primates. C.-H. CHIU¹, S.L. PAGE², and M. GOODMAN². ¹Dept. of Evolutionary Genetics, Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany and ²Dept. of Anatomy and Cell Biology, Wayne State University School of Medicine, Detroit, MI. chiu@eva.mpg.de

Investigations on the evolution of fetally expressed γ -globin genes in New World monkeys (platyrrhines) have yielded insights into the molecular evolutionary patterns and processes that have shaped the primate genome. Cladistic branching patterns of platyrrhines were reconstructed using nucleotide sequences of the tandemly duplicated γ -globin genes (5- $\gamma 1$ - $\gamma 2$ -3') that have not undergone gene conversions and are within non-coding regions. Results support a monophyletic platyrrhine clade. Within Platyrrhini, different species for the same genus always grouped together, as demonstrated by results on *Cebus* (capuchin m.), *Saimiri* (squirrel m.), and *Aotus* (night m.). There was strong support for the clade formed by *Callicebus* (titi m.) and *Chiropotes* (saki m.), a clade represented by *Ateles* (spider m.), and for the clade formed by *Callithrix* (marmoset), *Aotus*, *Saimiri*, and *Cebus*. In contrast to several independent lines of evidence, the γ data weakly supported a clade formed by *Aotus* and *Saimiri* and a clade formed by *Callithrix* and *Cebus*.

We mapped onto this framework of platyrrhine branching patterns dynamic changes in the structure and expression of the fetally expressed γ genes. Most notably, we observed that in platyrrhines, $\gamma 2$ is the primary fetal gene and $\gamma 1$ is either non-expressed or silent. In contrast, catarrhines (Old World monkeys and hominoids) have two functional genes, with $\gamma 1$ preferentially expressed. We placed these findings in a larger context of primate evolution and proposed a model that accounts for how γ acquired a novel (fetal) expression pattern and why different fetal patterns were maintained in platyrrhines and catarrhines. The γ gene

system may serve as a model for understanding aspects of genome evolution that underlie spatial and temporal shifts in gene expression through time.

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Is there life after 40? Implications of bone remodeling in African-Americans. H. CHO, University of Missouri, Columbia, MO 65211.

Previous research (Cohn et al. 1977, DeSimone et al. 1989, Nelson et al. 1991) indicates that ethnicity has an effect on bone remodeling rates and age-associated bone loss. Although it has been reported that European- and African-Americans have similar onsets of age-associated bone loss, the rate of bone loss decreases in African-Americans from the fourth decade onward compared to European-Americans (Garn et al. 1976). In a few bone remodeling studies (Frost 1987; Stout and Paine 1994; Wu et al. 1970), an osteon population density (OPD) asymptote is reported to occur around the fifth decade of life in the middle third of the rib. An OPD asymptote occurs when the entire cortex is occupied by osteons and each new osteon removes the evidence of previous ones (Frost 1987).

Histological analysis of 104 African-American mid-shaft ribs (mean age=52.84 years) resulted in a continuous increase in the number of osteons with age. The African-American sample appeared to lack an OPD asymptote. It is suggested that this reflects a slower bone remodeling rate and greater bone mass in African-Americans than their European-American counterparts.

These results support observations that African-Americans enjoy a higher quality and quantity of bone throughout old age and are significantly less susceptible to osteopenia and related fractures.

Isonymy in Kings County, NY, 1698-1810. A.F. CHRISTENSEN, Rutgers University, Camden, NJ 08102.

Isonymy has proved a useful method for studying the genetic structure of historical populations in the United States and elsewhere in the world. In the US, the populations studied have been of predominantly British origin. Many of the early settlers in this country, however, came from different cultural backgrounds, which may have affected their settlement patterns and genetic structure. The first European settlers of Kings County, New York, were Dutch, and Dutch was still spoken there in the nineteenth century. In the early Colonial period, it was an isolated

agricultural area, but it was increasingly drawn into the larger New York City, a process which culminated at the end of the nineteenth century. This paper uses census data from 1698, 1739, 1790, and 1810 to assess synchronic and diachronic isonymy patterns within the county. These censuses subdivide the county into six towns, five founded by the Dutch (Brooklyn, Bushwick, Flatbush, Flatlands, and New Utrecht) and one by the English (Gravesend). All were founded at least a generation before 1698. Values of I_{ii} , F_{ST} , and R_{ST} increased from 1698 to 1738, a period when Kings County received few immigrants, and decreased thereafter as the influence of the metropolis grew. Most new immigrants settled in Brooklyn, so the lowest levels of isonymy occurred there [I_{ii} (1810) = 0.0075]. The highest levels occurred in Gravesend, the English island within a Dutch sea [I_{ii} (1810) = 0.2094]. F_{ST} increased from 0.0114 to 0.0221, and then fell to 0.0175 and 0.0113; R_{ST} was approximately two-thirds as high, at 0.0078, 0.0161, 0.0121, and 0.0086. These levels are an order of magnitude higher than have previously been reported from nineteenth-century Massachusetts or Pennsylvania, and are comparable to those found in isolate populations. Correlations were sought between each sample's I_{ii} and the census population and number of surnames. The most significant correlation was that between I_{ii} and the number of surnames lost from that sample since the prior census. This is logical: those communities with the greatest continuity of names also exhibit the most isonymy.

Middle Pleistocene to Holocene postcranial gracilization in black wildebeest, *Connochaetes gnou*, and its implications for understanding diachronic changes in robusticity in the genus *Homo*. S.E. CHURCHILL¹, J.S. BRINK², and L.T. GRUSS¹, ¹Duke University, Durham, NC 27708 USA and ²National Museum, Bloemfontein, 9300 RSA.

It is well-established that postcranial robusticity decreased in members of the genus *Homo* from Middle Pleistocene to recent times. Explanations for this decrease have typically centered on temporal reduction in activity levels and mechanical loads on the skeleton, in the context of evolving cognitive, social, subsistence and technological systems. To determine if a Quaternary gracilization trend was unique to the genus *Homo*, we examined robusticity in a temporal series of black wildebeest, *Connochaetes gnou*, using geometric analysis of metapodial diaphyseal cross-sections. Data were collected on 159 individuals distributed among three temporal subspecies; the early Middle Pleistocene *C.g. laticornutus*, the late Middle and Late Pleistocene *C.g. antiquus*, and the Holocene *C.g. gnou*.

Body mass was estimated for each individual using articular dimensions and published regression equations. As with the genus *Homo*, black wildebeest experienced a reduction in average body mass from Middle Pleistocene to recent times (20.5-22.3%, compared to 14.3% in humans). Thus diaphyseal strength measures were standardized to body size by dividing by body mass for

measures of area and by (body mass * metapodial biomechanical length)^{1.33} for second moments of area.

Results reveal a diachronic reduction in metapodial robusticity comparable to that seen in the genus *Homo*. Size-standardized measures of diaphyseal resistance to axial loads decreased between 19.4 and 24.4%, while standardized measures of bending rigidity decreased between 32.7 and 44.1%. This reduction is equal to or greater than the amount of postcranial gracilization documented in the genus *Homo* across the Quaternary.

While we have no *a priori* reason to believe that the pattern seen in *C. gnou* holds for all mammals, these results do suggest that postcranial gracilization in humans may have been in response to ecological factors that were operating on other mammals as well.

Hominin bone accumulation at Zhoukoudian: The role of large carnivores. R. L. CIOCHON, Dept. of Anthropology, University of Iowa, Iowa City, IA 52242, N. T. BOAZ, Director of International Institute for Human Evolutionary Research, Bend, OR 97701, XU Qinqi, Director of Zhoukoudian International Research Center, IVPP, Box 643, Beijing, China and LIU Ginyi IVPP, Box 643, Beijing, China

The important fossil assemblage at Zhoukoudian has been hypothesized by various authors to have been accumulated by natural death of autochthonous species, by flowing water, by hunting activity of *Homo erectus*, and by scavenging activity of large carnivores, particularly hyaenids.

In this paper we review the evidence for each of these positions, and find that the preponderance of evidence supports the last alternative as the most important single taphonomic factor in the accumulation of the fossil assemblage at Zhoukoudian. Our conclusion that Zhoukoudian represents an alloped assemblage is supported by paleoecological evidence that argues against many of the mammalian species known from Zhoukoudian being considered as denizens of caves. A detailed consideration of the pattern of breakage of faunal remains, the pattern of body part representation, evidence of bite marks, evidence of hominin-derived cut marks, and a number of other measures of bone damage, suggest that most common species found at Zhoukoudian were prey species for large mammalian carnivores, particularly hyaenids. We then examine the hominin fossil record from Zhoukoudian, using all available casts and the few original fossils, to compare body part representation and the type of damage seen in the hominins with that of the general mammalian fauna.

This examination leads us to conclude that there is a close taphonomic match of the hominin assemblage and the general mammalian fauna from Zhoukoudian. Large mammalian carnivores are thus most likely responsible for accumulating the hominin sample at Zhoukoudian as well. In the light of this conclusion we re-evaluate the evidence for cannibalism at Zhoukoudian, and re-assess several behavioral interpretations long proffered for *Homo erectus*.

The Middle-Upper Paleolithic transition in western Eurasia. G.A. CLARK, Anthropology, Arizona State University, Tempe AZ 85287-2402

The dominant view of the Middle-Upper Paleolithic transition in western Eurasia is predicated on various construals of biological replacement (e.d., Mellars 1996), is embodied in the following six widely-reiterated 'textbook generalizations' (e.d., Tattersall 1998), and is seldom subjected to critical scrutiny.

There is supposedly (1) a shift in stone tool technology from technologies emphasizing the production of flakes (MP) to those emphasizing blades (UP); (2) an increase in the variety and complexity of stone tools involving more formal standardization in the various UP stages; (3) complex bone, antler and ivory artifacts appear with the earliest UP, and differentiate it from the MP; (4) an increase in the rate of change in lithic and bone technology, accompanied by more regional diversification of tool forms; (5) the first appearance of naturalistic or representational art along with a wide range of personal ornaments made from animal teeth, bone and marine shell, at the conventional M-UP boundary at c. 40 kya; and (6) associated changes in the social and economic organizations of human groups marked by (i) a more specialized pattern of animal exploitation, based on systematic hunting; (ii) a sharp increase in the overall density of human populations in some areas; (iii) an increase in maximum local group size, and (iv) the appearance of highly 'structured' sites, including more evidence for features.

These generalizations about the nature of pattern over the archaeological transition are reviewed for Europe and the Levant and are found to lack empirical support. Patterns in lithic technology, typology, raw material variability, reduction strategies, and site distributions indicate a temporal-spatial mosaic of changing monitors of human adaptation over the transition interval that cannot be reconciled with any construal of biological replacement. What we think of as paleolithic adaptations almost certainly constituted a range of options very broadly distributed in space and time, held in common by all circum-Mediterranean hominids, and invoked differentially according to context.

Behavior, Hormones, and Immune Correlates of Socially Stable/Unstable Housing in Juvenile Rhesus monkeys (*Macaca mulatta*). M. R. CLARKE, L. S. ANDERSON, J. PORTER, L. N. MARTIN. Dept. of Anthropology, Tulane University, New Orleans LA 70118, LSU School of Dentistry, and Tulane Primate Center.

Sixteen immature rhesus monkeys were studied from Nov 1995 to Oct 1996. After 2 months of baseline habituation, animals were transferred from outdoor corrals to indoor housing Jan 1996. Subjects were matched for sex, age, maternal history, baseline hormone and immune measures and were assigned randomly to the experimental (unstable) or control (stable) group. Four pairs remained stable, the others were paired randomly with different animals on Monday and separated on Friday. All animals had moving and fuzzy surrogate mothers, toys, and forage. Animals were bled at 4-week intervals, and 2

bleeds followed a potential environmental stressor, i.e. animal technicians entering the room with catch gloves and waving toy animals. Behavioral observations consisted of focal sampling 2-3 times each week for activity, proximity, social interactions, and stereotypic behaviors. Differences were tested using 2-way analysis of variance with repeated measures.

Unstable pairs clung more frequently to each other ($p < .02$), played more ($p = .02$), and groomed less ($p < .04$) than stable pairs. Unstable pairs exhibited stereotypic behaviors longer ($p < .04$), and interacted with the moving surrogate more frequently ($p < .001$) and longer ($p < .001$) than stable pairs. CD4, CD4/CD29, total CD8, CD20, and CD8/CD16 subsets showed increases over time, while Norepinephrine (NE), Epinephrine (EP) and Dopamine (DA) decreased over time. NE and DA also showed significant interaction effects. During the planned "stressors", stable controls exhibited higher NE and DA than their matched experimental animals, suggesting that capture behavior was not stressful to animals reorganized twice a week. NE and DA increased in the predicted direction during 2 other sample periods. Once the primary caretaker was on vacation, and once it was difficult to bleed the animals. In both cases, unstable pairs exhibited NE and DA concentrations that were triple the control pairs. These results confirm previous findings and provide insight into what provokes a "stress" response in a juvenile rhesus monkey.

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What the StW 573 *Australopithecus* skeleton reveals about early hominid bipedalism. R.J. CLARKE, Institut der Anthropologie und Humangenetik für Biologen, J.W. Goethe-Universität, Frankfurt am Main, Germany and Sterkfontein Research Unit, Dept. of Anatomical Sciences, University of the Witwatersrand Medical School, Johannesburg, South Africa.

Bipedalism as a habitual method of terrestrial locomotion is not unique to humans and their ancestors. It is the method used by birds and was used by many dinosaurs. Most birds, however, also use their forelimbs for flight and some use their hindlimbs for swimming as well as walking. Thus indications of bipedalism in hominid fossil lower limbs do not preclude the possibility of arboreal efficiency involving also the forelimbs. *Australopithecus* could well have been both biped and arboreal climber and this could only be determined with the discovery of a skeleton with associated fore- and hindlimbs, including feet and hands. Such a skeleton has recently been discovered in a 3.3 m.y. old deposit at Sterkfontein caves, South Africa. Preliminary assessment indicates that the foot had both bipedal and climbing capabilities, whilst the arm and hand indicate adaptation to arboreal locomotion. This skeleton's foot morphology is consistent with the bipedal Laetoli footprint trails, which are not those of fully human feet, but which have very clear ape-like morphology.

Paying the price of speech? An analysis of mortality statistics for choking on food.

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The low position of the human larynx is unique among mammals. The descent of the larynx is regarded as essential to our ability to produce the sounds of speech. It has, however, long been assumed that there is a price to pay for our ability to speak, in an increase in the risk of choking to death on the food we eat. This is because all food must pass across the laryngeal opening rather than stream round an upright epiglottis, as the epiglottis in humans is no longer in contact with the soft palate, as in human infants and all other mammals. If we are indeed at increased risk of choking as this hypothesis suggests, human deaths from choking on food should be high. One would also expect to see increases in the number of deaths from this cause at the stages in life when the larynx is descending to its adult position, in early childhood and at puberty. The largest numbers of deaths would therefore be expected in the 1-4 year olds and the early teenage years. Using mortality statistics for England & Wales taken from the last 100 years (1894-1994) it was found that overall mortality from choking on food was very low averaging 0.6 per 100,000 head of population. Furthermore, the rate in the groups predicted to be most vulnerable had some of the lowest numbers and rates of death. The analysis suggests that the risk of choking on food is related to co-ordination of swallowing and other risk factors.

Cranial growth in extant African apes. S. COBB and P. O'HIGGINS, Evolutionary Anatomy Unit, University College London, London, UK.

The combination of anatomical similarities and size differences in the crania of extant African apes has led some researchers to consider the differences in adult morphology a result of ontogenetic scaling. This study analyses the 3 dimensional growth of the cranium to ascertain the extent to which ontogenetic scaling is responsible for the differences in size and shape of extant African ape adult crania. 53 cranial landmarks (predominantly facial and basal) were collected from the sexed crania of *Gorilla gorilla gorilla* (62 adult; 75 subadult), *Pan troglodytes troglodytes* (58 adult; 57 subadult) and *Pan paniscus* (34 adult; 61 subadult). The 3 dimensional data for all three species is examined to compare ontogenetic shape and size changes using geometric morphometric techniques. Thus data are first registered using generalised Procrustes analysis and then patterns of ontogenetic scaling are examined using Principal components analysis (PCA) and by computing angles between growth vectors. The significance of these

angles is assessed using a permutation test. This methodology allows the shape variation during growth to be visualised and compared between species. Analyses of each species alone indicate that in all cases the first principal component (PC) adequately represents the shape changes occurring during growth in that scores on this PC are highly correlated with changes in size. No other PC shows significant correlation with size. Computation of the angles between these first PCs from each species indicate subtle and significant interspecific differences in the ontogeny of cranial shape. Despite this a combined analysis of all species indicates that they share important aspects of cranial growth but that there are sufficient differences to discount the hypothesis that interspecific differences in adult form are explained by relative extension or truncation of ontogenetic trajectories. The use of geometric morphometric methods in this analysis offers the advantage over conventional analyses of interlandmark distances that growth vectors can be both statistically compared and fully visualised using wireframe and rendered computer models.

Clades and Hominid Postcranial Fossils. K.E. COFFING and H.M. McHENRY. Department of Anthropology, University of California, Davis, CA 95616.

There is power and clarity in cladistic methodology, yet its application is not always convincing. This study explores both the promise and problems of applying cladistic methodology to hominid postcranial anatomy.

Craniocental characters are most commonly used in hominid cladistic analyses because of their more frequent preservation and more secure taxonomic identity. Postcranial characters, however, may also hold phylogenetic promise, providing researchers recognize the potential problems. The hominid fossil record is becoming complete enough to attempt to follow postcranial transformations among species of early hominid.

Our strategy for trait selection utilized both breadth (skeletal element coverage) and depth (many traits for best-known elements). This study uses 86 postcranial characters gathered from personal observations and the literature. Hominid species with sufficient published and available data include *Australopithecus anamensis*, *A. afarensis*, *A. africanus*, *Paranthropus robustus*, *Homo habilis sensu stricto*, *H. erectus/ergaster*, and *H. sapiens*. *Pan troglodytes* serves as the outgroup.

The five most parsimonious cladograms contain the branching sequence *P. troglodytes*-*A. anamensis*-*A. afarensis*-[*H. habilis* s.s. + *A. africanus*+*P. robustus*]-*H. erectus/ergaster*-*H. sapiens*. The order of the three species within brackets fluctuated, while the species outside the brackets did not. The results show significant postcranial similarities between early hominids and *H. habilis* s.s.

Problems in cladistic analyses, and particularly of postcrania, can arise from many sources, and thus the results must be treated with caution. Many hominid postcrania are less securely attributed to particular species than are craniodental remains. Characters may be correlated by developmental or functional relationships not yet understood. The skeletal elements of some hominid species are not yet represented in others. Parts of the body may change at unequal rates. The possible existence of significant homoplasy in the hominid fossil record makes phylogenetic analysis more complex.

Our results support the observation that there were two major steps in hominid postcranial evolution: first, early

bipedalism that was kinetically and energetically different from that of *H. sapiens* with retention of traits related to climbing (*Australopithecus* and *H. habilis*), and second, human bipedalism (*H. erectus/ergaster* and later *Homo*).

This research was supported by a University of California President's Postdoctoral Fellowship (K.C.) and the Committee on Research, UC Davis (H.M.).

Outline-based morphometrics and shape variation in the primate mandibular condyle. TM COLE III, University of Missouri, Kansas City, MO 64108; CE WALL, Duke University, Durham, NC 27710.

Outline-based morphometrics are useful for describing and comparing biological shapes when few or no homologous anatomical landmarks are available. There are a number of methods available for studying outlines, including Fourier analyses and eigenshape analysis. However, these methods have important assumptions and limitations. As an alternative, we consider a new method that was introduced in 1998 by CR Rao. Rao's method has several qualities that may make it preferable to other methods in many morphological comparisons. It is based on theories of circular vectors and is both coordinate-system and starting-position invariant.

We first demonstrate how the method identifies the optimal correspondence between two outlines. We then show how a generalized algorithm can be used to compare multiple specimens. Finally, we show how the method may have potential for "localization" of shape differences in exploratory studies (as long as the assumptions are made clear).

In an applied example, we use Rao's method for a study of shape variation in the primate mandibular condyle. Condylar outlines (superior view) are compared for 16 anthropoid taxa. After achieving a generalized alignment, we use principal coordinates analysis to summarize patterns in the data. The first two principal axes explain more than 90% of the variation in shape. The first axis separates the great apes and humans from the lesser apes and monkeys. The primary distinguishing feature of the great apes and humans is a relative expansion of the condyle's lateral pole. The second axis separates African apes and humans from *Pongo*, with the differences lying in the curvatures of the anterior and posterior margins.

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HUMAN FOREARM MUSCLE ARCHITECTURE. JM COLLACO and SW SIMPSON, Department of Anatomy, School of Medicine, Case Western Reserve University, Cleveland, OH 44106.

Muscle architecture is an important determinant of muscle function. Previous studies have examined relationships between muscle function and its architectural components (pennation and shape) using

gross dissection and/or medical imaging. Muscle shape is commonly characterized as a single variable, usually maximum fiber length or total muscle mass/volume. Similarly, fiber pennation in a muscle is often characterized as a single value - the average pennation angle. This study examines the relationships between muscle architecture and function in the primary human wrist muscles using higher resolution data for both shape and pennation.

The method adopted here calculates relative force and absolute excursion by modeling individual muscles as a series of stacked conic sections, each frustum with its own pennation. Measurements for this study were made on hand and forearm muscles of embalmed cadavera (CWRU School of Medicine human anatomy laboratories; n=8 [4♂, 4♀]) through gross dissection. To model the frustra, pennation and circumference were measured every 1 cm down the length of each antebrachial muscle. Additional observations including muscle lengths, total and free tendon lengths, minimum tendon circumference, and a series of external and cross-sectional measurements of the upper limb bones were made.

Substantial variation in muscle organization and size was observed between individuals. Fiber organization, which has a strong impact on muscle function, varied greatly within individual muscles suggesting single summary descriptive values of muscle architecture may be insufficient in modeling their function. Also, the relationship between maximum force, excursion, and pennation demonstrates that most muscles in the forearm have constrained force output secondary to the need for tendon excursion. Among the major wrist flexors and extensors, the M Flexor Carpi Ulnaris demonstrates a distinct fiber organization. As a consequence of its greater pennation, it is capable of a greater force output than the other primary wrist musculature. This may be related to the increased range of motion in wrist adduction or enhanced power grip seen in hominoids.

Ontogeny and homoplasy in the papionin face.

M. COLLARD and P. O'HIGGINS, University College London, WC1E 6BT, UK.

Recent studies indicate that adult extant papionins exhibit numerous craniodental homoplasies. Knowledge of how these similarities emerge through development is crucial for understanding the morphological evolution of the papionins. Accordingly, we have used geometric morphometric techniques to investigate papionin facial ontogeny.

The data set comprised 3-D landmark co-ordinates recorded on mixed-sex, growth series from five papionin genera. Thirty one landmarks were employed. The genera sampled were *Cercocebus*, *Lophocebus*, *Macaca*, *Mandrillus* and *Papio*.

Non-shape differences were removed by Generalised Procrustes Analysis. The shape data were subject to Principal Components Analysis (PCA) in the tangent space to Kendall's shape space. Principal component (PC) scores were plotted against centroid size to examine size related shape changes. As PC1 was found to adequately describe growth related changes in facial shape, the angles between

PC1s were used to estimate the degree of similarity of growth vectors. A further analysis examined the affinities among estimated average juvenile specimens of fixed size using PCA, distance matrices and phenograms. Lastly, the angles between growth vectors, and the PCAs and phenograms, were compared with the tribe's consensus molecular phylogeny (Harris and Disotell, 1998).

The analyses indicate that juvenile facial morphology is consistent with the molecular phylogeny in separating *Macaca* from the other papionins. However, the growth vectors, and the facial morphology of juveniles within the mangabey and baboon group, are not congruent with the molecular phylogeny. Thus, the facial homoplasies of the adult papionins are manifest in the growth vectors of their faces, and in younger age groups.

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Nuclear DNA variation of Aldolase A intron V in *Ateles*. A.C. COLLINS, Department of Anthropology, University of Wisconsin - Milwaukee and University of Wisconsin - Waukesha, Milwaukee, WI. 53201.

The goal of this research was to determine phylogenetic relationships among geographically and taxonomically distinct haplotypes of spider monkeys (*Ateles*) based on sequence variation of a nuclear DNA region. The Aldolase A intron V region was selected for this investigation. The phylogenetic relationships based on this nuclear DNA region were compared to previous phylogenies determined based on mitochondrial DNA variation.

Samples from all previously recognized species and most recognized subspecies of *Ateles* were sequenced, ranging from Central America throughout the Amazon Basin, to determine phylogenetic relationships among racially recognized groups. Comparison of DNA sequences based on both parsimony analysis and genetic distance analysis produced phylogenetic relationships that were similar.

The phylograms produced, along with associated bootstrap support, and confidence probabilities were analyzed. Support for the four previously proposed monophyletic species of *Ateles*, based on mitochondrial DNA variation, was demonstrated. Minor discrepancies between mitochondrial and nuclear phylogenies were attributable to differences in sample size and degree of sequence variation between mitochondrial and nuclear DNA regions.

The four species were as follows: *Ateles paniscus*, composed of haplotypes from the northeastern Amazon Basin; *A.belzebuth* found in the southern Amazon Basin; *A.hybridus* located primarily along the Magdalena River valley of Colombia; and *A.geoffroyi* which includes the two former species *A.geoffroyi* and *A.fusciceps*. Nuclear DNA corroboration of the mitochondrial DNA phylogenies provides additional support for suggested revisions in *Ateles* taxonomy as proposed by Collins and Dubach (accepted for pub). The proposed species are contradictory to long-held taxonomies based on pelage variation, and are instead similar to results proposed by Froehlich et al. (1991) based on cranio-dental variation.